

axmi007	-----MNQNNNNEYEIIDSKNLSYPSNRNIDHSRYPYTNNPNQPLQNTNYKEWLNMCQGN	55
cry1Aa	-----MDNNPNINECIPYN---CLSNPE-----	VEVL 24
cry1Ac	-----MDNNPNINECIPYN---CLSNPE-----	VEVL 24
cry1Ia	-----MKLKNQDKHQSFSNAVKDKISTDS---LKNETDIELQNIHEDCLKMSEYE	49
cry3Aa1	MIRKGGRKMNPNRSEHDTIKTTENEVPTNHVQYPLAETPNPTLEDLNYKEFLRMTADN	60
cry3Ba	MIRMGGRKMNPNRSEYDTIKVTPNSELPTNHNQYPLADNPNSTLEELNYKEFLRMTADN	60
cry4Aa	-----MNPYQNKNEYETLNASQKKNISN---NYTRYPIENSPKQLLQSTNYKDWLNCQQN	54
cry6Aa	-----	
cry7Aa	-----MNLNNLD--GYEDSNRTLNNSLNYP---TQKALSPSLKNMNYQDFLSITERE	47
cry8Aa	-----MSPNNQNEYEIIDATPSTSVDSDNRYPFANEPTDALQNMNYKDYLKMSGGE	52
cry10Aa	-----MNPYQNKNEYEIFNAPSNGFSKSN---NYSRYPLANKPNQPLKNTNYKDWLNCQDN	54
cry16Aa	-----MHYYGNRNEYDILNASSNSNMSN---TYPYPLANPQQDLMQNTNYKDWLNCCEGY	54
cry19Ba	-----MNSYQNKNEYEILDAKRNTCHMSN---CYPKYPPLANPQMYLRNTHYKDWINMCEEA	54
cry24Aa	-----MNQYQNKNEYEILESSQNNMNMPN---RYPFADDPNAVMKNGNYKDWFVNECEGS	51

axmi007	TQYGDNFETFASADTIAAVSAGTIVSGTLLAGIGGLTSISGPIGIIGAIISFGTLITVF	115
cry1Aa	G-----GERIETGYTPIDISLSTQFLLSEF-VPGAGFVLG-----LVDIIWGF	68
cry1Ac	G-----GERIETGYTPIDISLSTQFLLSEF-VPGAGFVLG-----LVDIIWGF	68
cry1Ia	N-----VEPFVS-ASTIQTGIGIAGKILGTLGVFAGQVAS-----LYSFILGEL	93
cry3Aa1	N-----TEALDSSTTKDVIQKGISVVGDLGVGVGFPGALVS-----FYTNFLNTI	107
cry3Ba	S-----TEVLDSSSTVKDAVGTVGIVGQILGVGVGVFAGALTS-----FYQSFLNAI	107
cry4Aa	QQYGGDFETFIDSG---ELSAYTIVVGTVLGFTTPLG-----LALIGFTLIPVL	104
cry6Aa	-----MIIDSKTTLPRHSLIHTIKLNSNKKYGPDMTN-----GNQFIIS	40
cry7Aa	Q-----PEALASGNTAINTVSVTGATLSALGVPGASFITN-----FYLKIAGLL	92
cry8Aa	NP-ELFGNPETFIS-SSTIQTGIGIVGRILGALGVFASQIAS-----FYSFIVGQL	102
cry10Aa	QQYGNNAGNFASSETIVGVSAGIIVVGTMLGAFAAPVLAAG-----IISFGTLLPIF	106
cry16Aa	H-----IENPREASVRAGLKGKLGIVSTIVGFFGGSIILDIG-----LFYQISELL	101
cry19Ba	S-----YASSGPSQL---FKVGGSIVAKILG-----MIPEVGP-----LLSWMVSLF	93
cry24Aa	N-----ISPSPAAITSKIVSIVLKTAKAVASSLAD-----SIKSSLG	90

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axmi007	WPAGEQDKTVWTQFIKMGEIFVDTPLTESIKQLKLQTLEGFRQILQ---SYNTALDDWRK	172
cry1Aa	GPS---Q---WDAFPVQIEQLINQRRIEEFARNQAISRLEGLSNLYQ---IYAESFREWEA	119
cry1Ac	GPS---Q---WDAFLVQIEQLINQRRIEEFARNQAISRLEGLSNLYQ---IYAESFREWEA	119
cry1Ia	WP---KGKNQWEIFMEHVEEIINQKISTYARNKALTDLKGGLDALA---VYHDSLESWVG	147
cry3Aa1	WPS---E---DPWKAFMQVEALMDQKIADYAKNKAELQGLQNNVE---DYVSALSSWQK	160
cry3Ba	WPS---DA-DPWKAFAQVEVLIDKKIEEYAKSKAELQGLQNNFE---DYVNALDSWKK	161
cry4Aa	FPAQDQS-NTWSDFITQTKNIIKKEIASTYISNANKILNRSFNVIS---TYHNLKTWE-	159
cry6Aa	KQE-----WATIGAYIQTGLGLPVNEQLRTHVNLSQDISIPSDFSQLYDVYCS---	89
cry7Aa	WPE--NGKI-WDEFMTEVEALIDQKIEEYVRNKAIAELDGLGSALD---KYQKALADWLG	146
cry8Aa	WPS--KSVDIWGEIMERVEELVDQKIEKYVKDKALAAELKGLGNALD---VYQQSLEDWLE	157
cry10Aa	WQGSDPA-NVWQDLLNIGGRPIQ-EIDKNIINVLTISIVTPIKNQLD---KYQEFFDKWEP	161
cry16Aa	WPEDDTQQYTWQDMMHVEDLIDKRITERVIRGNAIRTLADLQGKVD---DYNNWLKKWKD	158
cry19Ba	WPTIEEKNTVWEDMIKYVANLLQKELTNDLNRATSNLGLNESLN---IYNRALAAWKQ	150
cry24Aa	ISKTITENNVSQVSMVQVHQIINRRIQETILDGESSLNGLVAIYNR---DYLGALEAWN	148

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Fig. 1A

axmi007	LKRLQAPGLPPSSALQQAALT	KIRFENVHND	FIREIPG	--FQLETYK	TL	LLPIYA	QAAN	230																																					
cry1Aa	-----DPTN	-----PALREEMRI	QFN	DMNS	SALT	TAI	PL	LA	VQ	QAAN	166																																		
cry1Ac	-----DPTN	-----PALREEMRI	QFN	DMNS	SALT	TAI	PL	FAV	-----	NYQVPLLSVYVQ	QAAN	166																																	
cry1Ia	-----NRNN	-----TRAR	SVVKSQYIA	ELMFVQ	KLPS	FAVS	-----	GEEV	PL	PIYA	QAAN	194																																	
cry3Aa1	-----NPVSSRNPHS	QGR	I	ELFS	SQA	ESH	F	RNS	MPS	FAIS	-----	GYEV	FL	TTY	QAAN	210																													
cry3Ba	-----APVNLRSRRS	QDR	I	ELFS	SQA	ESH	F	RNS	MPS	FAVS	-----	KF	EVL	FL	PTY	QAAN	211																												
cry4Aa	-----NNPNPQNT	QD	V	R	T	Q	I	Q	L	V	H	F	Q	N	V	PEL	V	N	C	P	S	D	C	D	Y	Y	N	I	L	V	S	S	Y	Q	A	A	215								
cry6Aa	-----DKTSAEWWNK	N	L	Y	PL	I	I	K	S	A	D	I	AS	Y	-----	G	F	K	V	A	G	D	P	S	I	K	D	G	-----	129															
cry7Aa	-----KQDD	-----PEA	I	LSV	A	T	F	R	I	D	S	L	F	E	F	S	M	P	S	F	K	V	T	-----	GYE	I	P	L	L	T	V	Y	Q	A	A	193									
cry8Aa	-----NRND	-----AR	TR	S	V	S	N	Q	F	I	A	D	L	N	F	V	S	S	I	P	F	A	V	S	-----	G	H	E	V	L	L	A	V	Y	Q	A	V	N	204						
cry10Aa	-----ARTHANAKA	V	H	D	L	F	T	T	L	E	P	I	D	K	D	L	M	L	K	N	-----	N	A	S	Y	R	I	P	T	L	P	A	Y	A	Q	I	A	208							
cry16Aa	-----DPK	S	T	G	N	L	S	T	L	V	T	K	F	T	A	L	D	S	F	N	G	A	I	R	T	V	N	N	Q	G	S	P	-----	GYE	Y	LL	LL	P	V	Y	A	Q	I	A	208
cry19Ba	-----NKNNFAS	G	E	L	I	R	S	Y	I	N	D	L	H	I	F	T	R	D	I	Q	S	D	F	S	L	G	-----	GYE	T	V	L	L	P	S	Y	A	S	A	198						
cry24Aa	-----NKS	N	I	Y	Q	T	N	V	A	E	A	F	K	T	V	E	R	F	F	T	K	L	K	G	I	Y	R	T	S	-----	SSQ	I	T	LL	P	T	F	Q	A	A	196				

axmi007	FHLNLLQQGAELA	DE	W	N	A	D	I	H	P	S	Q	I	E	P	N	A	G	T	S	D	Y	Y	K	-	LL	K	E	N	I	P	K	S	N	Y	C	A	N	T	Y	R	E	G	L	289
cry1Aa	LHLSVLRDVS	V	F	G	Q	R	W	G	F	D	A	-----	-----	AT	I	N	S	R	N	D	L	T	R	L	I	G	N	Y	T	D	Y	A	R	W	Y	N	T	G	LE	216				
cry1Ac	LHLSVLRDVS	V	F	G	Q	R	W	G	F	D	A	-----	-----	AT	I	N	S	R	N	D	L	T	R	L	I	G	N	Y	T	D	Y	A	R	W	Y	N	T	G	LE	216				
cry1Ia	LHLLLRLDAS	I	F	G	K	E	W	G	L	S	S	-----	-----	SE	I	S	T	F	Y	N	R	Q	V	E	R	A	G	D	Y	S	D	H	C	V	W	Y	S	T	G	LN	244			
cry3Aa1	THLFLLKD	A	Q	I	Y	G	E	E	W	G	Y	E	-----	-----	ED	I	A	E	F	Y	K	R	Q	L	K	L	T	Q	Y	T	D	H	C	V	W	N	V	G	LD	260				
cry3Ba	THLLLKL	D	A	Q	V	F	G	E	E	W	G	Y	SS	-----	-----	ED	I	A	E	F	Y	Q	R	Q	L	K	L	T	Q	Y	T	D	H	C	V	W	N	V	G	LD	261			
cry4Aa	LHLT	V	L	N	Q	A	V	K	F	E	A	Y	L	K	N	R	Q	F	D	Y	L	P	-	TA	I	D	Y	T	N	C	V	T	T	Y	K	G	LN	273						
cry6Aa	-YFKKLQ	D	E	L	D	N	I	V	D	N	S	D	-----	-----	DA	I	A	K	A	I	K	D	F	K	A	R	G	I	L	I	K	E	A	K	Q	171								
cry7Aa	LHLALLR	D	S	T	L	Y	G	D	W	G	F	T	Q	-----	-----	NN	I	E	Y	N	R	Q	K	E	Y	S	D	H	C	V	N	S	G	LS	243									
cry8Aa	LHLLLRLDAS	I	F	G	E	E	W	G	F	T	-----	-----	GE	R	C	V	254																											
cry10Aa	WHLNLLKHA	A	T	Y	N	I	W	Q	N	---	Q	265																																
cry16Aa	LHLLLRLD	A	Q	I	Y	G	D	K	W	S	A	-----	-----	AN	A	R	D	N	Y	Y	Q	I	Q	L	E	K	T	Y	E	C	I	259												
cry19Ba	LHLLLRLD	V	A	I	Y	G	-	K	E	L	G	Y	-----	-----	STD	V	E	F	Y	Y	Q	K	Y	T	E	K	S	N	Y	C	V	N	T	Y	K	G	LE	248						
cry24Aa	LHLSMLRDAV	M	Y	Q	E	G	W	N	L	Q	S	-----	-----	HIN	Y	S	K	E	L	D	A	L	E	Y	T	N	C	V	E	V	Y	T	K	G	LN	244								

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axmi007	KLRNEP	-----	N	M	R	W	S	I	F	D	Y	R	R	M	T	I	T	V	L	D	T	I	A	Q	F	S	Y	D	I	K	R	K	S	I	G	R	I	G	K	I	T	E	L	T	343	
cry1Aa	RVWGPDS	-----	R	D	W	V	R	Y	N	Q	F	R	R	E	L	T	L	T	V	L	D	I	A	V	F	N	S	Y	D	S	R	R	Y	R	Y	P	-----	IRTVSQLT	264							
cry1Ac	RVWGPDS	-----	R	D	W	V	R	Y	N	Q	F	R	R	E	L	T	L	T	V	L	D	I	A	V	F	N	S	Y	D	S	R	R	Y	R	Y	P	-----	IRTVSQLT	264							
cry1Ia	NLRGTNA	-----	E	S	W	V	R	Y	N	Q	F	R	R	E	M	T	L	M	V	L	D	L	V	A	L	F	P	S	D	T	Q	M	Y	-----	I	K	T	A	Q	L	T	292				
cry3Aa1	KLRGSSY	-----	E	S	W	V	N	R	Y	R	R	E	M	T	L	T	V	L	D	L	I	A	L	F	P	L	Y	D	V	R	Y	P	-----	K	E	V	K	T	E	L	T	308				
cry3Ba	SLRGSTY	-----	D	A	W	V	K	F	N	R	F	R	R	E	M	T	L	T	V	L	D	L	I	V	F	P	L	Y	D	V	R	Y	P	-----	K	G	V	K	T	E	L	T	309			
cry4Aa	LIKTTPD	S	N	L	D	G	N	N	W	N	T	Y	N	T	Y	R	T	K	M	T	A	V	L	D	L	V	A	L	F	P	N	Y	D	V	G	K	Y	-----	I	G	V	S	E	L	T	327
cry6Aa	YEEAAKN	-----	I	V	T	S	L	D	Q	F	L	H	G	D	Q	K	-----	H	222																											
cry7Aa	RLNGSTY	-----	E	Q	-----	M	-----	291																																						
cry8Aa	KLKGTT	-----	K	S	-----	M	-----	302																																						
cry10Aa	MIRTNT	-----	N	-----	I	313																																								
cry16Aa	DFRTAGQ	-----	W	-----	E	305																																								
cry19Ba	SKKQIG	-----	W	-----	I	298																																								
cry24Aa	ALRGSTA	-----	I	-----	L	292																																								

Fig. 1B

axmi007	REIYTTEINFDRLTYL-----EIOPNLAIMEYNLTRSGLRLFSFLDELIFYTKNETYG	396
cry1Aa	REIYTNPVLENFDGS-----FRG--MAQRIEQNIRQPHLMDILNSITIYTDVHRGF	313
cry1Ac	REIYTNPVLENFDGS-----FRG--SAQGIERSIERSPHLMDILNSITIYTDHRY	313
cry1Ia	REVTDAIGTVPHPSFTSTTWYNNNAPSFSAAEAVVRNPHLLDFEQVTIYSL-----R	350
cry3Aa1	RDVLTDPIVGNNLR-----GYGTTFSNIEN-YIRKPHLFYDYLHRIQFHTRFQPGY	358
cry3Ba	RDIFTDPIFTLNALQ-----EYGPFTFSSIEEN-SIRKPHLFYDYLRGIEFHTRLRPGY	359
cry4Aa	REIY-QVLNFEESPYK-----YYD--FQYQEDSLTRR-PHLFTWLDSLNFYEKAQTP	376
cry6Aa	KELLEKVKNLKTTLER-----TIKAEQDLEKKVEYSFLLGPLLGFVVYEILEN	270
cry7Aa	REVYTDPVSLISNP-----DIGPSFSQMENTAIRTPHLVDYLDELYIYTSKYKAF	342
cry8Aa	RDVYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNIRPPHLFDILSSVEINTSRGGIT	362
cry10Aa	REVY---TNVNSDTFR-----TIT---ELENGLTRN-PTLFTWINQGRFYTRNSRDI	358
cry16Aa	REIYSDVINGEYGLM-----TPYFSFEKAESLYTRA-PHLFTWLKGFRFVTNSISYW	357
cry19Ba	REIYSDVINDHVYGLM-----VPYISFEHAESLYTRR-PHAFTWLKGFRFVTNSINSW	350
cry24Aa	RKIYDTPVGRTDSPSGF-DWTNTGRTLANFNDLEREVTDSPSLVKWLGDMTIYTGAIDSY	351
	...	
axmi007	NRLVGIAN-RNRSTYATTGTEIIYGERTGPPTT-KTLIPFESYKVSIVTDRQVTPTSPFP	454
cry1Aa	N-----YWSGHQITASPVGFGSGPEFAFPFLFGNAGNAAPP-VLVSLLTGLGIFRTLSSP	364
cry1Ac	Y-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS	365
cry1Ia	WSNTQYMN-MWGGHKLEFRTIGTTLNISTQ---GSTNTSINPVTLPPFTSRDVYRTESLA	405
cry3Aa1	YGNDSFN--YWSGNVYSTRPSIGSNDIITSFSPFYGNKSEPVQ--NLEFNGEKVVYRAVANT	414
cry3Ba	SGKDSFN--YWSGNVYETRPSIGSNDIITSFSPFYGDKSIEPIQ--KLSFDGQKVYRTIANT	415
cry4Aa	NNFFTSHY-NMFHYTLDNISQKSSVFGNHNVTD-KLSSLGLATNIYIFLNNVISLDNKYL	434
cry6Aa	TAVQHIKN--QIDEIKKQLDSAQHDLRDVKIIGMLNSINTDIDNLYSQGQEAIKVFQKL	328
cry7Aa	SHEIOPDLYWSAHKVSFKKSEQSN-LYTTCIYGTSGYISS-GAYSFHGNDIYRTLAAP	400
cry8Aa	LNNDAYIN-YWSGHTLKYRRTADSTVTVTA---NYGRITSEKNSFALEDRDIFEINSTV	417
cry10Aa	LDPYDIFS-FTGNQMAFTHTNDRNIIWGAHNG-NIISQDTSKVFYRNKPIDKVEIVR	416
cry16Aa	TFLSGGQN-KYSYTN-NSSINEGSFRGQDTDYGGTSSTINIPNSNSYVYNLWTENYEIYP	415
cry19Ba	TFLSGGEN-RYFLTHGEHTIYNGPFLGQDTEYGGTSSYIDISNNNSIYNLWTKNYEIYP	409
cry24Aa	RPTSPGDRIGWYGNINAFYHTGRDVMFRQTDAYEDPSTFISNILYDDIYKLDLRA	411
axmi007	N-IYFTINQIELYLNNSP--SNKLTYSGGNLSNDKTTDFQFPVKKDCKPII--NPNCL	509
cry1Aa	---LYRRIILGSGPNNQELFVLDGTEFSFASLTTLPSTIYRQRTVDSLVIIPPQDNSV	421
cry1Ac	---LYRRPFN-IGINNQQLSVLGTEFAYG-TSSNLPSSAVYRKSGTVDSLDEIPPQNNNV	420
cry1Ia	GLNLFLTQPVNGVPRVDFHWKFVTHPIASDNFYPGYAGIG--TQLQDSENELPPEATGQ	463
cry3Aa1	NLAWWP-SAVYSGVTKVEFSQYNDQTDIAESTQTYDSKRN-VGAV-SWDSIDQLPPETTDE	471
cry3Ba	DIAAFPDGKIYFGVTKVDFSQYDDQNETSTQTYDSKRY-NGYLGQAQDSIDQLPPETTDE	474
cry4Aa	N-DYNNISKMDFFITNGTRLLEKELTAGSGQITYDVNKNIFGLPILKRRENQG--NPTLF	491
cry6Aa	QGIWATIGAQIENLRTSLQEVQDSDADEIQUIELEDASDAWLVAQEARD-----	379
cry7Aa	SVVVVYPQTQN-YGVEQVEFYGVKGHVHYRGDNKYDL-----TYDSIDQLPPDGE	448
cry8Aa	ANLANYYQKAYGVPGSWFHMVKRGTSSTAYLYSKTHTALQGCTQVYESDEIPLDRT-V	476
cry10Aa	HREYSDIIYEMIFFNSSS--EVFRYSSNSTIENNYKRTDSYMPKQTWKN-----	464
cry16Aa	WGDPVNITKMNFSVTDNN--SSKELIYGAHRTNKPVVRTDFDFTLNKEGTE-----L	465
cry19Ba	WTDPVNITKINFSTDNS--NSSESIYGAERMNKPVRTDFNLLNRAGNG-----P	459
cry24Aa	AAVSTIQGAMDTTFGVSSSRFFDIRGRNQLYQSNKPYPSLPIITFPGEESSE-----	464

Fig. 1C

axmi007	PSYNNSYSHILSQFSLFNYSYKIGLALNILYTGALGUTHSSVRNNAI SDKIITMIPA IKG	569
cry1Aa	PPRAGFSHRLSHVTMLSQAAG---AVTLLRAPTFSWQHRSAEFNNIIPSSQITQIPLTKS	478
cry1Ac	PPRQGFSHRLSHVSMFRSGFSNS-SVSIIRAPMF SWIHRSAE FNNIIASDSITQI PAVKG	479
cry1Ia	PNYESYSHRLSHIGLISASHVK--ALVYS-----WTHRSADRTNTIEPNSITQIPLVKA	515
cry3Aa1	PLEKGYSQHQLNYVMCFLMQGSR-----GTIPVLTWTHKSVDFFNMIDS KITQLPLVKA	525
cry3Ba	PLEKAYSHQLNYAECFLMQDRR-----GTIPFFT WTHRSVDFNTIDA EKITQLPVVKA	528
cry4Aa	PTYDNYSHILSFIKSL SIP-----ATYKTQVYTFAWTHSSVDPKNTIYTHLTTQI PAVKA	546
cry6Aa	-----FTLNAYSTNSRQNL PINVISDSCNCST	406
cry7Aa	PIHEKYTHRLCHATAIFKSTP---DYDNATIPIFSWTHRSAEYYNRIYPN KITKIPAVKM	505
cry8Aa	PVAESYSHRLSHITSHFSKNG---SAYYGSFPVFVWTHTSADLNNTIYSD KITQI PAVKG	534
cry10Aa	---EYGHHTLSYIKTDNYIFS---VVRERRVAFSWTHTSVDFQNTIDLDN ITQIHALKA	518
cry16Aa	AKYNDYNHILSYMLINGETFG---QKRHGYSAFTHSSVDPNNTIAANKITQI PAVKA	520
cry19Ba	TTYNDYNHILSYMLINGETFG---QKRHGYSAFTHSSVDRYNTIVPD KIVQI PAVKT	514
cry24Aa	GNANDYSHLLCDV KILQEDSSN-ICEGRSSLLSHAWTHASLDRNNTILPDEITQI PAVTA	523

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axmi007	NSLDTNSKVIEGPGHTGGNLVYLQSQGR-----LEITCRTPNSTQSYYIRLRYATNGA	622
cry1Aa	TNLGSGTSVVKGPGFTGGDILRRTSPQI STLRVNITAPL-----SQRYRVRIRYASTTN	533
cry1Ac	NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF PSTSTRYRVRVRYASVTP	538
cry1Ia	FNLSSGAAVVRGPGFTGGDILRRTNTGTFGDIRVNINPPF-----AQRYRVRIRYASTTD	570
cry3Aa1	YKLQSGASVVAGPRFTGGDIIQCTENG---SAATIYVTP-DVSYSQKYRARIHYASTSQ	580
cry3Ba	YALSSGASIIIEGPGFTGGNLLFLKESSN---SIAKFVTLNSAALLQRYRVRIRYASTTN	585
cry4Aa	NSLGTASKVVQGP GHTGGDLIDFKDH-----FKITCQHSNFQQSYFIRIRYASNGS	597
cry6Aa	TNMTSNQYSNPTTNMTS-----NQYMISHEYTSLPN	437
cry7Aa	YKLDDPSTVVKGPGFTGGDLVKGSTGYIGDIKATVNSPL-----SQKYRVRVRYATNVS	560
cry8Aa	DMLYLGGSVVQGP GFTGGDILKRTNPSILGTFAVTVNGSL-----SQRYRVRIRYASTTD	589
cry10Aa	LKVSSDSKIVKGPGHTGGDLVILKDSMD-----FRVRFLKN-VSRQYQVRIRYATNAP	570
cry16Aa	SSINGSISIEKGPGFTGGDLVKMRADSG-----LTMRFKAE LLKKYRVRIRYKCNYS	573
cry19Ba	NLVG--ANIKGP GHTGGDLLKLEYERF-----LSLRIK-LIASMTFRIRIRYASNIS	564
cry24Aa	YELRGNSSVVAGPGSTGGDLVKMSYHS-----WWSFKVYCSELKNYRVRIRYASHGN	575

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axmi007	GNTLPNISLTIPGVIGIP PQRLNNFTSGTNYNNLQYGDGFYFQFPSTVTLPLNR--NIPF	680
cry1Aa	LQFH TSIDGRPINQGNFS-----ATMSSGSNLQSGSFRTVGFTTPFNFNSNGS---SVF	583
cry1Ac	IHLNVNWGNSSIFSNTVP-----ATATSLDNLQSSDFGYFESANAFTSSLGN-----	585
cry1Ia	LQFH TSINGKAINQGNFS-----ATMNRGEDLDYKTFRTVGFTTPFSLDVQ---STF	620
cry3Aa1	ITFTLSDGAPFNQYYFD-----KTINKGDTLTYSNFSNLASFSTPFELSG-----NNL	628
cry3Ba	LRLFVQNSNNDFLVIYIN-----KTMNIDGDLTYQT FDFATNSNSNMFGSGDT---NDF	635
cry4Aa	ANTRAVINL SIPGVAELG-MALNPTFSGTDYTNLKYKDFQYLEFSNEVKFAPNQ--NISL	654
cry6Aa	NFMLS RNSNLEYKCPENN-----FMIYWYNNSDWYNNSDWYNN-----	475
cry7Aa	GQFNVYINDKITLQTKFQN---TVETIGEGKDLTYGSFGYIEYSTTIQFPDEH--PKI	613
cry8Aa	FEFTLYLG-DTIEKNRFN-----KTMMDNGASLT YETFKFASFITDFQFRETO---DKI	638
cry10Aa	KTTVFLT GIDTISVELPS---TTSRQNPNA TDLTYADFGYVTFPRTVPNKT FEGEDTLL	626
cry16Aa	SKLILRKWKGEFYIQQQI-----HNISPTYGAFSYLESFTITTENIFDLTME-VTYPY	626
cry19Ba	GQMMINIGYQNPTYFNII-----PTTSRDYTELK-FEDFQLVDTSYIYSGGPS-ISS--	614
cry24Aa	CQFLMKRWPSTGVAPRQWAR---HNVQGTFNSNSMRYEAFKYLDIFTITPEENN F-----	626

Fig. 1D

axmi007	IFNRADVSN-SILIIDKIEFIPITSSVRQNREKQKLETIQTAKINTFFTNTKNTLNIEAT	739
cry1Aa	TLSAHVNSGNEVYIDRIEFVPAEVTFEA---EYDLERAQKAVNELFTSSNQIGLKTDTV	640
cry1Ac	IVGVRNFSGTAGVIIDRFEFIPVTATLEA---EYNLERAQKAVNALFTSTNQLGLKTNVT	642
cry1Ia	TIGAWNFSGGNEVYIDRIEFVPEVTYEA---EYDFEKAQEKTALFTSTNPRGLKTDVK	677
cry3Aa1	QIGVTGLSAGDKVYIDKIEFIPVN-----	652
cry3Ba	IIGAESFVSNEKIYIDKIEFIPVQ-----	659
cry4Aa	VFNRSVDVYTNTVLIDKIEFLPITRSIREDREKQKLETVQQIINTFYANPIKNTLQSELT	714
cry6Aa	-----	
cry7Aa	TLHLSDSLSSNNSFYVDSIEFIPVVDVNYAE---KEKLEKAQKAVNVLFT-GRNALQKDVT	669
cry8Aa	LLSMGDFSSGQEVYIDRIEFIPVDETYEA---EQDLEAAKKAVNALFTNTKD-GLRPGVT	694
cry10Aa	MTLYGTPNHSYNIYIDKIEFIPITQSVDYTEKQNIKTQKIVNDLFVN-----	675
cry16Aa	GRQFVEDIPS--LILDKIEFLPTN-----	648
cry19Ba	NTLWLDNFSNGPVIIDKIEFIPLGITLNQAQGYDTYDQNANGMYHQNYNSNGYNQEYN	674
cry24Aa	-AFTIDLESGGDLFIDKIEFIPVSGSAFEYEGKQNIKTQKAVNDLFIN-----	674
axmi007	NYDID-----	744
cry1Aa	DYHIDQVSNLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWR	700
cry1Ac	DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG	702
cry1Ia	DYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQLHIERNM-----	719
cry3Aa1	-----	
cry3Ba	-----	
cry4Aa	DYDIDQAANLVECISEELYPKEKMLLDEVKNAKQLSQSRNVLQNGDFE---SATLGWT	770
cry6Aa	-----	
cry7Aa	DYKVDQVSILVDCISGDLYPNEKRELQNLVKYAKRLSYSRNLLDPTFDSINSSEENGWY	729
cry8Aa	DYEVNQAANLVECLSDDLYPNEKRLFDAVREAKRLSGARNLLQDPDFQEING--ENGWA	752
cry10Aa	-----	
cry16Aa	-----	
cry19Ba	TYYQSYNN-----	682
cry24Aa	-----	

Fig. 1E